

FIG. 2B

Phe	Phe	Thr	Ser	Phe	Tyr	Trp	Ser	Phe	Ile	Thr	Thr	Met	Thr	Thr	Val	Gly	Phe	Gly	Asp	Leu
TTC	TTC	ACT	TCA	TTC	TAC	TGG	TCC	TTC	ATT	ACA	ATG	ACT	GTC	GGG	TTT	GGC	GAC	TTC	540	
Met	Pro	Arg	Arg	Asp	Gly	Tyr	Met	Tyr	Ile	Ile	Leu	Tyr	Ile	Ile	Leu	Gly	Lys	Phe	200	
ATG	CCC	AGA	AGG	GAC	GGG	TAC	ATG	TAT	ATC	ATA	TTG	CTC	TAT	ATC	ATT	TTA	GGT	AAA	TTT	600
Ser	Met	Lys	Lys	Phe	Lys	Ile	Phe	Leu	Gly	Leu	Ala	Ile	Thr	Thr	Met	Cys				
TCA	ATG	AAA	AAA	CAA	AAA	TTC	AAA	ATA	TTT	TTA	GGT	CTT	GCA	ATA	ACT	ACA	ATG	TGC	660	
Ile	Asp	Leu	Val	Gly	Val	Gln	Tyr	Ile	Arg	Lys	Ile	Tyr	Phe	Gly	Arg	Lys	Ile	Gln	240	
ATT	CAT	TTC	GTA	GGA	GTA	CAG	TAT	ATT	CGA	AAG	ATT	CAT	TAT	TTC	GGA	AGA	AAA	ATT	CAA	720
Asp	Ala	Arg	Ser	Ala	Leu	Ala	Val	Gly	Gly	Lys	Val	Val	Val	Ser	Glu	Leu	Tyr		260	
GAC	GCT	AGA	TCT	GCA	TTG	GCG	GTT	GTA	GGA	GGA	AAG	GTA	GTC	CTT	GTA	TCA	GAA	CTC	TAC	780
Ala	Asn	Leu	Met	Gln	Lys	Arg	Ala	Arg	Asn	Met	Ser	Arg	Glu	Ala	Phe	Ile	Val	Glu	Asn	280
GCA	AAT	TTA	ATG	CAA	AAG	CGA	GCT	CGT	AAC	ATG	TCC	CGA	TTA	GCT	TTT	ATA	GTG	GAG	AAT	840
Leu	Tyr	Val	Ser	Lys	His	Ile	Ile	Pro	Phe	Ile	Pro	Thr	Asp	Ile	Arg	Cys	Ile	Arg	Tyr	300
CTC	TAT	GTT	TCC	AAA	CAC	ATC	ATA	CCA	TTC	ATA	CCA	ACT	GAT	ATC	CGA	TGT	ATT	CGA	TAT	900
Ile	Asp	Gln	Thr	Ala	Asp	Ala	Ala	Thr	Ile	Ser	Ser	Ser	Ala	Ile	Asp	Met	Gln		320	
ATT	GAT	CAA	ACT	GCC	GAT	GCT	GCT	ACC	ATT	TCC	ACG	TCA	TCT	TCT	GCA	ATT	GAT	ATG	CAA	960
Ser	Cys	Arg	Phe	Cys	His	Ser	Arg	Tyr	Ser	Leu	Asn	Arg	Ala	Phe	Lys				336	
AGT	TGT	AGA	TTT	TGT	CAT	TCA	AGA	TAT	TCT	CTC	AAT	CGT	GCA	TRC	AAA	TAG	(SEQ 1) NO:3	(SEQ 1) NO:4	1011	

FIG. 3B

FIG. 4

(SEQ 1) NO. 7) MIRK
(SEQ 1) NO. 8) HRROMK1
(SEQ 1) NO. 9) RGIRK1
(SEQ 1) NO. 10) Dm H5-1

(SEQ 1) NO: 11) Shak
 (SEQ 1) NO: 12) Shal
 (SEQ 1) NO: 13) Shab
 (SEQ 1) NO: 14) Shaw
 (SEQ 1) NO: 15) Eag
 (SEQ 1) NO: 16) Slo
 (SEQ 1) NO: 17) Dm H5-2

(SEQ ID NO:18) Dm H5-1
 (SEQ ID NO:19) Ce 5-1
 (SEQ ID NO:20) Dm H5-2
 (SEQ ID NO:21) Ce H5-2

AFLFSIETQTTIGYGFRCVTDEC
AFLFSLETQVTIGYGFRCVTEQCA
AFLFFIETEATIGYGYRYITDHCP
...
AFFFRAFTVCSTVGYGNISPTTFA
...
AFWWAVVTMTTGVGDMDPTVGFWG
AFWYTIVTMTTLGYGDMDVPETIAG
AFWWAGITMTTGVGYGDICPTTALG
GLWWALVTTMTTGVGYGDMAKPTYIG
ALYFTMTCMTSVGFGNVAETDNE
CVYFLIVTMSVTGYGDVYCTVLG
...
SLYTSYVTTTIGFGDYYPTFGAN

$$\begin{cases} \{G, A, S, T\}, & \{D, E\} \\ \{N, Q\}, & \{K, R, H\} \\ \{F, Y, W\} = \{I, L, M, V\} \end{cases}$$

AAAAAFTVCSTVGYGNISPTTFA
SIFFAVTVTTIGYGNPVPVTNTG
SLYTSYVTTTIGFGDYVPTFGAN
SFYWSFITMTTVGFGDLMPPRDGY

FIG. 5A

230	Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu	240	250
	TAC CAC TAT CAC CAT CAA AAA GGA ATG GAA ATT CGC GAA AAG GCG GAA ACC GAC AGA CCG TCT CCA TCC ATT CTT		750
260	Trp Thr Thr Phe Thr Asn Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Ile Phe	270	
	TGG ACC ACA TTC ACA AAC TGT TAT GGG CAA CTC TTC AAT GTT TGG TTC TGC TTT GCC GTT ACT CTC ACA ATC TTC		825
280	Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly Phe Leu Asn Lys Ile Met Ser Glu Asn ASP Glu Ile	290	300
	CCT GTT ATG ATG ACC GTT ACC ACT CGT GGA GAT TCC GGC TTC CTA AAC AAA ATT ATG TCT GAA AAC GAT GAA ATC		900
310	Tyr Thr Leu Leu Thr Ser Phe Leu Val Phe Ala Ala Ile Gly Ser Ile Val Ala Ser Lys Ile His	320	
	TAC ACT TTG CTC ACA AGT TTC CTC GTC GTC AAT TTG TTC GCT GCG ATT GGA TCC ATA GTT GCT TCC AAC ATT CAC		
330	Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Phe Cys Asn	340	350
	TGG CCG ACA CCC CGT TAC CTC AAA TTT GCC ATA ATC TTG CGT CCT CTT TGC ATT CCA TTC TCC TTC TCC TGC AAC		975
360	Tyr Arg Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr ASP Ile Phe Val Ile Gly Gly Ile Ala Met	370	
	TAT CGT GTC CAG ACG CGT GCT TAT CCT GTT TCC TTT GAG TCT ACT GAC ATT TTT GTC ATT GGT GGA ATT GCC ATT		1125
380	Ser Phe Ser His Gly Tyr Leu Ser Ala Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg	390	400
	TCT TTT TCA CAT GGA TAC CTC AGC GCT CTC GCA ATG GGA TAC ACT CCA AAC GTC GTC CCA TCT CAC TAC TCA AGA		1200
410	Phe Ala Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr Gly Gly Ile Ile Glu	420	
	TTT GCC GCT CAG CTT TCC GTT TCC ACT CTT ATG GTT CGC CTT CTC ACC GGT GCC CTC TGG CCC GTT GTT ATT GAG		
430	His Phe Val Asp Lys Pro Ser Ile Leu (SEQ ID NO: 63)	434	1275
	CAC TTC GTG GAC AAG CCA ACT ATC TTA TAA ATTTATAGCTTACAGTCTTATCTTCTTCTTAACTGCTGGAAATA		1364
	ATATTATTA <u>AAAAAAAAAA</u> 1388 (SEQ ID NO: 36)		

FIG. 9B

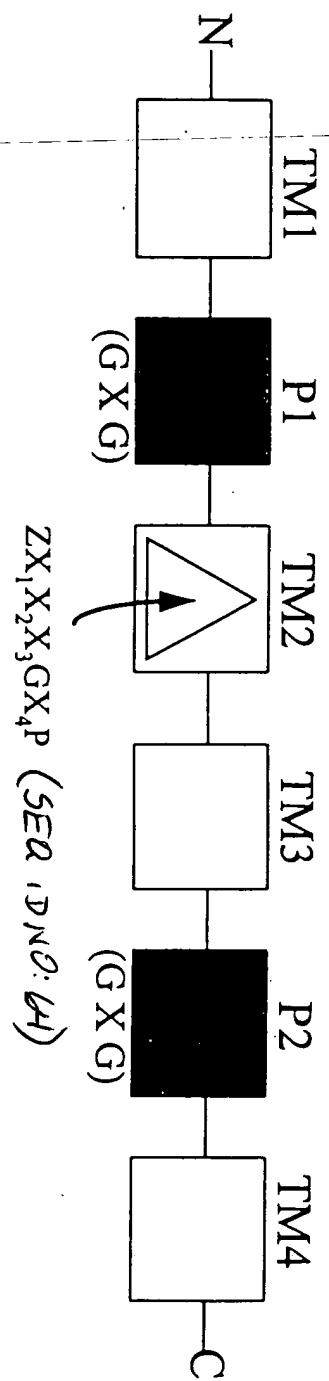


FIG. 10